SEQUENCE LISTING

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       Kulesza, Caroline A.
       Walters, Frederick S.
       Slatin, Stephen L.
       Von Tersch, Michael A.

<120> POLYPEPTIDE COMPOSITIONS TOXIC TO COLEOPTERAN INSECTS

<130> MECO:218--1 11792.0218.DVUS01

<150> 09/427,770
<151> 1999-10-27

<150> 08/993,722
<151> 1997-12-18

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<170> PatentIn version 3.2

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<213> Artificial sequence

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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat   96
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            20   25   30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
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gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
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aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca   336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100   105   110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt   384
Gln Val Glu Val Leu Ile Asp Lys Lys .Ile Glu Glu Tyr Ala Lys Ser
            115   120   125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat   432
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    130   135   140

gtt aat gcg tta aat tcc tgg aag aaa ttt cac cat tct cgt cgt tct   480
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aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt   528
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cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg   576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180   185   190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta   624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195   200   205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa   672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210   215   220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac   720
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225   230   235   240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga   768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
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ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa   816
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            260   265   270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat   864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275   280   285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att   912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290   295   300

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ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca    960
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305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat   1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt   1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga   1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
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cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat   1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt   1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
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tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag   1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
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gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa   1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
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aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc   1344
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His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa   1440
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            485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att   1536
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gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act    1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
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aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc    1776
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            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
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aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
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625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
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Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
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Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130         .   135             140

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His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

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225             230             235             240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
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Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
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Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
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Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
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Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
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Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
        420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
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Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr.Leu Asn Ser Ala
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Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat   96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20   25   30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35   40   45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat   192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50   55   60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
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65   70   75   80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85   90   95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca   336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100   105   110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt   384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115   120   125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat   432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130   135   140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt   480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt   528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165   170   175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg   576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180   185   190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta   624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu

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tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220

gat gtt gct gaa ttc ctt agt aga caa tta aaa ctt aca caa caa tac        720
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225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

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                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt       1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga       1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat       1152
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    370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt       1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag       1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa       1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430
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cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca        1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa        1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg        1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att        1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

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Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa        1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca        1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act        1728
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                565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc        1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca        1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag        1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc        1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                    1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
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His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
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Asp Val Ala Glu Phe Leu Ser Arg Gln Leu Lys Leu Thr Gln Gln Tyr
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            260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275   280   285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
290   295   300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
            370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405   410   415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435   440   445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450   455   460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465   470   475   480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485   490   495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500   505   510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515   520   525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530   535   540

```
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650
```

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<400>  5
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct    48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat    96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat   192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
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```
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct cca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Pro Glu
    210                 215                 220

gat gtt gct gaa ttc agt cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Ser His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290                 295                 300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
```

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat   1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325   330   335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt   1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340   345   350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga   1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                355   360   365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat   1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370   375   380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt   1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag   1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405   410   415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa   1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420   425   430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc   1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
                435   440   445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca   1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450   455   460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa   1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465   470   475   480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg   1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485   490   495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att   1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500   505   510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc   1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515   520   525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa   1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530   535   540

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gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca     1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act     1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc     1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca     1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag     1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc     1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                 1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650


<210>  6
<211>  652
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  6

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95
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```
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155                     160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Pro Glu
    210             215             220

Asp Val Ala Glu Phe Ser His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
    275             280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295             300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400
```

```
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
            610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210>   7
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 7
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct   48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat   96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20   25   30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35   40   45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat   192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50   55   60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85   90   95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca   336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100   105   110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt   384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115   120   125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat   432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130   135   140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt   480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt   528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165   170   175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg   576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180   185   190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta   624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu

```
tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa       672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220
```

```
gat gtt gct gaa ttc tat cgt aga caa tta aaa ctt aca caa caa tac       720
Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240
```

```
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga       768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250                 255
```

```
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa       816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270
```

```
atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat       864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285
```

```
att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att       912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300
```

```
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca       960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320
```

```
act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat      1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325                 330                 335
```

```
tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt      1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350
```

```
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga      1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365
```

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cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat      1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
            370                 375                 380
```

```
aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt      1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400
```

```
tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag      1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405                 410                 415
```

```
gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa      1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430
```

```
aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc      1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca      1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa      1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg      1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att      1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650
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<210>  8
<211>  652
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  8

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
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Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275   280   285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290   295   300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405   410   415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435   440   445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450   455   460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465   470   475   480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485   490   495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500   505   510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515   520   525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530   535   540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
              565   570   575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
              580   585   590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
          595   600   605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
      610   615   620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625   630   635   640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
              645   650

<210> 9
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 9
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct   48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat   96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20   25   30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35   40   45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat   192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50   55   60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu

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aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115             120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

gat gtt gct gaa ttc tat aat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr Asn Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

tct gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Ser Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290             295             300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320
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act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat    1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt    1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga    1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat    1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt    1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag    1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa    1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc    1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca    1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa    1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg    1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att    1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc    1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa    1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530             535             540
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gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650


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<212>   PRT
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85              90              95
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Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
            130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
            210                 215                 220

Asp Val Ala Glu Phe Tyr Asn Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Ser Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290                 295                 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400
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Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
             405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
             420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
             435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
             450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
             485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
             500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
             515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
             530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
             565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
             580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
             595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
             610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
             645             650
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<210> 11
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct          48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15


aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat          96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30


cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg         144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45


act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat         192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60


gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta         240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80


gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt         288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95


aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca         336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110


caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt         384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125


aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat         432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140


gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt         480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160


aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt         528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175


cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg         576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190


ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta         624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205
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tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

gat gtt gct gaa ttc tat acc aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr Thr Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat       1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt       1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga       1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat       1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt       1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag       1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa       1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430
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aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc      1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca      1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450                 455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa      1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg      1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att      1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650
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<210>   12
<211>   652
<212>   PRT
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220

Asp Val Ala Glu Phe Tyr Thr Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250                 255
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Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275   280   285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290   295   300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405   410   415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435   440   445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450   455   460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465   470   475   480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485   490   495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500   505   510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515   520   525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530   535   540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545   550   555   560

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Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
              565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
              580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
              595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
         610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
              645             650


<210>   13
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1956)

<400>   13
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct        48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat        96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
              20              25              30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg        144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
         35              40              45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat        192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta        240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt        288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
              85              90              95
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aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115             120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
            130             135             140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180             185             190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
            210             215             220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

att aat tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Asn Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290             295             300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320
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act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat        1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt        1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga        1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat        1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt        1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag        1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa        1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc        1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
                435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca        1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa        1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg        1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att        1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc        1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa        1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca        1680
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Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act    1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc    1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645             650
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<210> 14
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 14

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
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                100                     105                     110
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

Ile Asn Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
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Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
          420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
          435   440   445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450   455   460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465   470   475   480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
              485   490   495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
              500   505   510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
          515   520   525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530   535   540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545   550   555   560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
              565   570   575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
              580   585   590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
          595   600   605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610   615   620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625   630   635   640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
          645   650

<210> 15
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 15
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg     144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat     192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta     240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt     288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca     336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt     384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat     432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
            130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt     480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt     528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg     576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta     624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205
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tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa     672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac     720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga     768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa     816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat     864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att     912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

ttt acg gat cca att ttt tta ctt act acg ctt cag aag tac gga cca     960
Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat     1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt     1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga     1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat     1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt     1200
Lys Ser Thr Glu -Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag     1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa     1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc     1344
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Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca      1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa      1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg      1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att      1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>  16
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<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 16

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255
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Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro
305                 310                 315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410     ·             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435                 440                 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485                 490                 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
    ·       500                 505                 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520                 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530                 535                 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560
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Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
              565               570               575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
              580               585               590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
         595               600               605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
         610               615               620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625               630               635               640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
              645               650


<210> 17
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin


<220>
<221> CDS
<222> (1)..(1956)

<400> 17
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10               15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
              20               25               30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg     144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
         35               40               45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat     192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
         50               55               60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta     240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65               70               75               80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt     288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
              85               90               95
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aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115             120           .     125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
            130             135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165   .             170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180             185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
            210             215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245             250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260             265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290             295                 300

ttt acg gat cca att ttt acc ctt aat aca cta cag aag tgc gga cca        960
Phe Thr Asp Pro Ile Phe Thr Leu Asn Thr Leu Gln Lys Cys Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat       1008
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Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                 325                 330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt      1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
             340                 345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga      1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
             355                 360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat      1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
         370                 375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt      1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390             395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag      1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                 405             410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa      1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
             420                 425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc      1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
             435                 440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca      1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
         450                 455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa      1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg      1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                 485                 490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att      1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
             500                 505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
             515                 520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
         530                 535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
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gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act  .  1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc     1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca     1824 .
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag     1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
            610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc     1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                 1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650
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<210> 18
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 18

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110
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Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             .   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275             280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

Phe Thr Asp Pro Ile Phe Thr Leu Asn Thr Leu Gln Lys Cys Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
        340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415
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Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210> 19
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>

H: 532973(BF8T011.DOC)   50

<221> CDS
<222> (1)..(1956)

<400> 19
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct        48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat        96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg       144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat       192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta       240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt       288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca       336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt       384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat       432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt       480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt       528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg       576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta       624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa       672
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Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac    720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga    768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa    816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat    864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att    912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290             295             300

ttt acg gat cca att ttt gcc gtt aat act ctg tgg gaa tac gga cca    960
Phe Thr Asp Pro Ile Phe Ala Val Asn Thr Leu Trp Glu Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat   1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt   1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga   1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat   1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
            370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt   1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag   1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa   1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc   1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
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          435                    440                    445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca    1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa    1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg    1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att    1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc    1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa    1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca    1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act    1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc    1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>   20
<211>   652
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<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 20

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
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              260                 265                 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

Phe Thr Asp Pro Ile Phe Ala Val Asn Thr Leu Trp Glu Tyr Gly Pro
305                 310                 315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440                 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505                 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515                 520                 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530                 535                 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
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                565                      570                      575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                  585              590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595              600              605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610              615              620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625              630              635              640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645              650
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<210> 21
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 21

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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg     144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat     192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta     240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt     288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca     336
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Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105             110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt      384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat      432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135             140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt      480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150             155             160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt      528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg      576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta      624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200             205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa      672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215             220

gat gtt gct gaa ttc tat cgt aga caa tta aaa ctt aca caa caa tac      720
Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga      768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa      816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat      864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att      912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290                 295             300

ttt acg gat cca att ttt tta ctt act acg ctt cag aag tac gga cca      960
Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro
305                 310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat     1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
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tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt     1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                     345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga     1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                     360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat     1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
            370                     375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt     1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                     390                     395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag     1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                     410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa     1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                     425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc     1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435                     440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca     1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450                     455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa     1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                     470                     475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg     1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                     490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att     1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                     505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc     1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                     520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa     1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530                     535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca     1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                     550                     555                 560
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gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act        1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc        1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca        1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag        1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc        1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                    1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>  22
<211>  652
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  22

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110
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Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro
305                 310                 315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
        340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405                 410                 415
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Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435   440   445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450   455   460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465   470   475   480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485   490   495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500   505   510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515   520   525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530   535   540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545   550   555   560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565   570   575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580   585   590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595   600   605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610   615   620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625   630   635   640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645   650

<210> 23
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS

<222> (1)..(1956)

<400> 23
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct        48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat        96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg       144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat       192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta       240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt       288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca       336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt       384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat       432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt       480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt       528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg       576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta       624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa       672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
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gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac      720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga      768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa      816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat      864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att      912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290             295             300

ttt acg gat cca att ttt acg cca acc acc cta cag gat tac gga cca      960
Phe Thr Asp Pro Ile Phe Thr Pro Thr Thr Leu Gln Asp Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat     1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt     1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga     1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat     1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt     1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag     1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa     1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc     1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445
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cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca        1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa        1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg        1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att        1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc        1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa        1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca        1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act        1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc        1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca        1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag        1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc        1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                    1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210>   24
<211>   652
<212>   PRT

<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 24

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270
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Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275             280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290             295             300

Phe Thr Asp Pro Ile Phe Thr Pro Thr Thr Leu Gln Asp Tyr Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
        420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575
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Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
        580                     585                 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>   25
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1956)

<400>   25
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct       48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat       96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg      144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat      192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta      240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt      288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca      336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
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caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt      384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat      432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt      480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt      528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg      576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta      624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa      672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac      720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga      768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa      816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat      864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att      912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

ttt acg gat cca att ttt gcc ctg aat acc tta gac gag tac gga cca      960
Phe Thr Asp Pro Ile Phe Ala Leu Asn Thr Leu Asp Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat     1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335
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tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt        1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga        1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat        1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt        1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag        1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa        1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc        1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca        1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa        1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg        1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att        1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc        1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa        1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca        1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560
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gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act     1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc     1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca     1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag     1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc     1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630·                635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                 1959 ·
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>  26
<211>  652
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  26

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
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Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130   135   140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165   170   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
        180   185   190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
        245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
        260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275   280   285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290   295   300

Phe Thr Asp Pro Ile Phe Ala Leu Asn Thr Leu Asp Glu Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
        325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
        340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
        405   410   415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln

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              420                    425                    430
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                440                445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                455                460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                470                475                480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                490                495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                505                510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515                520                525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530                535                540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                550                555                560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565                570                575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                585                590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                600                605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                615                620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                630                635                640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                650


<210>   27
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1956)
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<400> 27

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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct        48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat        96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg       144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat       192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta       240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt       288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca       336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt       384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat       432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt       480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt       528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg       576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta       624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa       672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220
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gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac          720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga          768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                    245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa          816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tac gat          864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285

act agg cga ttc aga aag ggg gtt aaa aca gaa cta aca aga gac att          912
Thr Arg Arg Phe Arg Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca          960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat         1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                    325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt         1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga         1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat         1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt         1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag         1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                    405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa         1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc         1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435                 440                 445
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cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca       1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa       1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg       1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att       1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500             505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc       1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa       1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca       1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act       1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc       1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca       1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag       1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc       1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                   1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210> 28
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223>   Recombinant delta endotoxin

<400>   28

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20   25   30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35   40   45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50   55   60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85   90   95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100   105   110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115   120   125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130   135   140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165   170   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180   185   190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260   265   270

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Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

Thr Arg Arg Phe Arg Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405                 410                 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
        420                 425                 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440                 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485                 490                 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500                 505                 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515                 520                 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530                 535                 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565                 570                 575
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Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
        580                 585                 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>  29
<211>  1959
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin


<220>
<221>  CDS
<222>  (1)..(1956)

<400>  29
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct       48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat       96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg      144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat      192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta      240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt      288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca      336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110
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caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115             120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180             185             190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
            210             215             220

gat gtt gct gaa ttc tat cgt aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290             295             300

ttt acg gat cca att ttt tta ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Leu Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat       1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325             330             335
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tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt     1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga     1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat     1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
            370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt     1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag     1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa     1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc     1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca     1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa     1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg     1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att     1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc     1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa     1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca     1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act     1728
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Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
             565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc    1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
             580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
             595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
             610             615             620     ·

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
             645             650


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<211>  652
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  30

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
             20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
             35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
             50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
             85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
             100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
             115             120             125
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Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165             170             175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275             280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

Phe Thr Asp Pro Ile Phe Leu Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
        340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
    355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
        420             425             430
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Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
        580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
        645             650
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<210>   31
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1956)
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct        48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat        96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg       144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat       192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta       240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt       288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca       336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt       384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat       432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt       480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt       528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg       576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta       624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa       672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220
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gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac          720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                     230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga          768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                    245                 250                 255

ggt tca act tat gat·gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa          816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat          864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att          912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290                 295                 300

ttt acg gat cca att ttt atc ctc aat acg cta cag gag tac gga cca          960
Phe Thr Asp Pro Ile Phe Ile Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat         1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt         1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga         1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat         1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt         1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag         1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410 ·               415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa         1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc         1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg· cca gaa aca aca         1392
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His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa    1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg    1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att    1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc    1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa    1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca    1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act    1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc    1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>  32
<211>  652
<212>  PRT
<213>  Artificial sequence
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<220>
<223> Recombinant delta endotoxin

<400> 32

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20   25   30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35   40   45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50   55   60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85   90   95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100   105   110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115   120   125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130   135   140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165   170   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180   185   190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
    195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp

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                275                         280                         285
    Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

    Phe Thr Asp Pro Ile Phe Ile Leu Asn Thr Leu Gln Glu Tyr Gly Pro
    305                 310                 315                 320

    Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                    325                 330                 335

    Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                    340                 345                 350

    Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                355                 360                 365

    Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370                 375                 380

    Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
    385                 390                 395                 400

    Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                    405                 410                 415

    Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420                 425                 430

    Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
                435                 440                 445

    His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450                 455                 460

    Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
    465                 470                 475                 480

    Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                    485                 490                 495

    Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

    Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515                 520                 525

    Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

    Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
    545                 550                 555                 560

    Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

    Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
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Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650
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<210>   33
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1956)

<400>   33
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg     144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat     192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta     240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt     288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca     336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110
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```
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt    384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat    432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt    480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt    528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg    576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta    624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa    672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac    720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga    768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa    816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat    864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att    912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

ttt acg gat cca att ttt atc cta cat acg ctg cag gag tac gga cca    960
Phe Thr Asp Pro Ile Phe Ile Leu His Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat    1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt    1056
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Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340               345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga    1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355               360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat    1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
            370               375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt    1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385               390           .   395                   400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag    1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405               410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa    1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420               425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc    1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435               440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca    1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450               455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa    1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465               470               475                   480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg    1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485               490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att    1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500       .       505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc    1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515               520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa    1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530               535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca    1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545               550               555                   560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act    1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
```

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aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc    1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
        580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650
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<210> 34
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 34

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125
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Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165             170             175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

Phe Thr Asp Pro Ile Phe Ile Leu His Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430
```

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Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650


<210>   35
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1956)

<400>   35
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct          48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat          96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg         144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat         192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta         240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt         288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca         336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt         384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat         432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt         480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt         528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg         576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta         624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa         672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac         720
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Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga      768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa      816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat      864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att      912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290             295             300

ttt acg gat cca att ttt tcc ctc gtt aac cta atg gtg tac gga cca      960
Phe Thr Asp Pro Ile Phe Ser Leu Val Asn Leu Met Val Tyr Gly Pro
305             310             315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat     1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt     1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga     1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat     1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt     1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag     1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa     1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc     1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca     1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
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        450                    455                    460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa   1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg   1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                        485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att   1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                    500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc   1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa   1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca   1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act   1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc   1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca   1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag   1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc   1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa              1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650


<210>   36
<211>   652
<212>   PRT
<213>   Artificial sequence

<220>
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<223> Recombinant delta endotoxin

<400> 36

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20   25   30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35   40   45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50   55   60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85   90   95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100   105   110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115   120   125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130   135   140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165   170   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180   185   190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275   280   285

```
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300
```

```
Phe Thr Asp Pro Ile Phe Ser Leu Val Asn Leu Met Val Tyr Gly Pro
305             310             315             320
```

```
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335
```

```
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350
```

```
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365
```

```
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380
```

```
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400
```

```
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415
```

```
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430
```

```
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445
```

```
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460
```

```
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480
```

```
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495
```

```
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510
```

```
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525
```

```
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530             535             540
```

```
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560
```

```
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575
```

```
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590
```

```
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645             650
```

<210> 37
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 37
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg     144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat     192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta     240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt     288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca     336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt     384
```

```
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
    115             120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat      432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt      480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt      528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165             170             175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg      576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
        180             185             190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta      624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195             200             205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa      672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac      720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga      768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa      816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat      864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att      912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

ttt acg gat cca att ttt tct ctt agg aca cca ctt gcg tac gga cca      960
Phe Thr Asp Pro Ile Phe Ser Leu Arg Thr Pro Leu Ala Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat     1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt     1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
```

```
ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga    1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat    1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt    1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag    1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa    1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc    1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca    1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa    1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg    1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att    1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc    1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa    1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca    1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act    1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575
```

```
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
            610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650


<210>  38
<211>  652
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  38

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
```

```
        130                      135                      140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

Phe Thr Asp Pro Ile Phe Ser Leu Arg Thr Pro Leu Ala Tyr Gly Pro
305                 310                 315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
```

```
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505                 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520                 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530                 535                 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650
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<210> 39
<211> 1959
<212> DNA
<213> Artificial sequence
<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 39
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15
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```
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat        96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
        20              25              30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg        144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat        192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50              55              60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta        240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt        288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130             135             140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165             170             175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210             215             220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240
```

```
act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga      768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa      816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt ttc aat      864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Phe Asn
            275             280             285

att ttg ctt tac agt aaa ggg gtt aaa aca gaa cta aca aga gac att      912
Ile Leu Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290             295             300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca      960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat     1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt     1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga     1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat     1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt     1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag     1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa     1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc     1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca     1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa     1440
```

```
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg     1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att  ·  1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500             505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc     1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa     1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca     1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act     1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc     1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca     1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag     1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
            610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc     1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645             650


<210>   40
<211>   652
<212>   PRT
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin

<400>   40
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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165             170             175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
    195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Phe Asn
    275             280             285

Ile Leu Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300
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Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr·Phe
            340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605
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Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>   41
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1956)

<400>   41
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct       48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat       96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg      144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
                35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat      192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
            50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta      240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt      288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca      336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt      384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
                115                 120                 125
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aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

att gtg tta tac·tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Val Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat        1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt       1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga       1104
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Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
    355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat   1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt   1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag   1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa   1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc   1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
                435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca   1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa   1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg   1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att   1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc   1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa   1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca   1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act   1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc   1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
```

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tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa               1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650
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<210> 42
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 42

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
            130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
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Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                    165   170   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                    180   185   190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
                    195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                    245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                    260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
                    275   280   285

Ile Val Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290   295   300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                    325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                    340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                    355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                    405   410   415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                    420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
                    435   440   445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr

```
        450                    455                    460
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470                 475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505                 510          ·

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515                 520                 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585                 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650

<210>    43
<211>    1959
<212>    DNA
<213>    Artificial sequence
<220>
<223>    Recombinant delta endotoxin


<220>
<221>    CDS
<222>    (1)..(1956)

<400>    43
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
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cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg        144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                      40                      45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat        192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                      55                      60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta        240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                      70                      75                      80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt        288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                      90                      95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                     105                     110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                     120                     125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                     135                     140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                     150                     155                     160

aaa aga agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                     170                     175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                     185                     190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
                195                     200                     205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                     215                     220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                     230                     235                     240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                     250                     255
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ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290             295             300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat       1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt       1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga       1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355             360             365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat       1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt       1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag       1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa       1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc       1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca       1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa       1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480
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tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg      1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490             .       495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att      1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635             .       640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650
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<210> 44
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 44

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1                   5                   10                  15
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
            50                  55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115                 120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150                 155                 160

Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290             295                 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310                 315                 320
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Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405                 410                 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435                 440                 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485                 490                 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505                 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520                 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530                 535                 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565                 570                 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620
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Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625   630   635   640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645   650

<210>   45
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin

<220>
<221>   CDS
<222>   (1)..(1956)

<400>   45
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct   48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat   96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20   25   30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35   40   45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat   192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50   55   60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85   90   95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca   336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100   105   110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt   384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115   120   125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat   432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130   135   140

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gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga aat          480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn
145                 150                 155                 160

cca cac agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt          528
Pro His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                    165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg          576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                    180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta          624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
                    195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa          672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac          720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga          768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                    245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa          816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                    260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat          864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
                    275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att          912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca          960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat         1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                    325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt         1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                    340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga         1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                    355                 360                 365
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cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat     1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt     1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag     1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa     1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc     1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca     1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa     1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg     1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att     1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc     1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa     1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca     1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act     1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc     1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca     1824
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Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210> 46
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 46

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
        20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn
145             150             155             160

Pro His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
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His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
    180   185   190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
    195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
  210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
    245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
    260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
    275   280   285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
  290   295   300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
    325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
    340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
    355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
  370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
    405   410   415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
    420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
    435   440   445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450   455   460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu

```
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                490                495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                505                510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515                520                525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530                535                540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                550                555                560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                570                575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                585                590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                600                605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                615                620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                630                635                640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                650
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<210> 47
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 47
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct    48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1                5                10                15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat    96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                25                30
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cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg      144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat      192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta      240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt      288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca      336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt      384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat      432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt      480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt      528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg      576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta      624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa      672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac      720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga      768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250                 255
```

```
ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
        260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

gtt cgg tta tac cca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat       1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt       1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga       1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat       1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt       1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag       1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa       1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc       1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca       1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa       1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg       1488
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      Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                      485                 490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att          1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc          1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520                 525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa          1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca          1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act          1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc          1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca          1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595                 600                 605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag          1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc          1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                      1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>  48
<211>  652
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  48

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15
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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
         20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
         35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55      .              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
             85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185     .           190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320
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Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
610 615 620

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Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625               630               635               ‘    640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
              645               650
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<210> 49
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956) .

<400> 49
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct        48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat        96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg       144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35              40              45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat       192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50              55              60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta       240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt       288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca       336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt       384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat       432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130             135             140
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gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga aat          480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn
145               150               155               160

cca cac agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt          528
Pro His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                  165               170               175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg          576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
              180               185               190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta          624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
          195               200               205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa          672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
      210               215               220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac          720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225               230               235               240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga          768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                  245               250               255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa          816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
              260               265               270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat          864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
          275               280               285

gtt cgg tta tac cca aaa ggg gtt aaa aca gaa cta aca aga gac att          912
Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
      290               295               300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca          960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305               310               315               320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat         1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                  325               330               335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt         1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
              340               345               350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga         1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
          355               360               365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat         1152
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Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370               375               380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt      1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385               390               395               400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag      1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405               410               415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa      1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420               425               430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc      1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435               440               445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca      1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450               455               460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa      1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465               470               475               480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg      1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485               490               495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att      1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500               505               510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515               520               525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530               535               540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545               550               555               560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565               570               575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580               585               590

tac att aat aaa act atg àat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
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ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650
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<210> 50
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 50

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
        20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
        85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
        100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn
145             150             155             160

Pro His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175
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His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180              185              190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195              200              205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
            210              215              220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230              235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245              250              255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260              265              270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275              280 ·             285

Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290              295              300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310              315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325              330              335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340              345              350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                355              360              365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
370                 375              380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390              395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405              410              415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420              425              430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
                435              440              445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450              455              460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470              475                 480
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Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515                 520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550             555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                 585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630             635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650

<210>   51
<211>   1956
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1953)

<400>   51
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct        48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat        96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg       144
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40              45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat        192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55              60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta        240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70              75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt        288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gaa gac cca tgg aag gct ttt atg gca caa        336
Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln
                100                 105                 110

gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt aaa        384
Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys
            115                 120                 125

gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat gtt        432
Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val
        130                 135                 140

aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt aaa        480
Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser Lys
145                 150                 155                 160

aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt cat        528
Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
                165                 170                 175

ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg ctg        576
Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu
                180                 185                 190

ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta tta        624
Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu
                195                 200                 205

aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa gat        672
Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp
        210                 215                 220

gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac act        720
Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr
225                 230                 235                 240

gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga ggt        768
Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly
                245                 250                 255

tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa atg        816
Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met
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act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat att        864
Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile
        275             280             285

cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att ttt        912
Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe
        290             295             300

acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca act        960
Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr
305             310             315             320

ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat tat       1008
Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr
                325             330             335

tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt ggg       1056
Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly
                340             345             350

aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga cct       1104
Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro
        355             360             365

agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat aaa       1152
Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys
        370             375             380

tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt tat       1200
Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr
385             390             395             400

cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag gta       1248
Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val
                405             410             415

tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa aaa       1296
Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys
                420             425             430

aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc cat       1344
Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His
        435             440             445

gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca gat       1392
Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp
        450             455             460

gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa tgt       1440
Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys
465             470             475             480

ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg aca       1488
Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr
                485             490             495
```

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cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att act      1536
His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr
            500             505             510

caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc att      1584
Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile
            515             520             525

att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa gaa      1632
Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu
    530             535             540

tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca gcc      1680
Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala
545             550             555             560

ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act aac      1728
Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn
            565             570             575

tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc tac      1776
Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr
            580             585             590

att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca ttt      1824
Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe
            595             600             605

gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag aat      1872
Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn
    610             615             620

gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc tat      1920
Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr
625             630             635             640

ata gat aag ata gaa ttt atc cca gta caa ttg taa                      1956
Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210> 52
<211> 651
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 52

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                      40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                      55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                      70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln
            100                 105                 110

Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys
        115                 120                 125

Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val
        130                 135                 140

Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser Lys
145                 150                 155                 160

Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
            165                 170                 175

Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu
            180                 185                 190

Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu
            195                 200                 205

Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp
        210                 215                 220

Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr
225                 230                 235                 240

Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly
            245                 250                 255

Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met
            260                 265                 270

Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile
            275                 280                 285

Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe
        290                 295                 300

Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr
305                 310                 315                 320

Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr
                325                 330      ·          335
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Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly
            340                 345             350

Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro
        355             360             365

Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys
    370             375             380

Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr
385             390             395             400

Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val
            405             410             415

Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys
            420             425             430

Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His
        435             440             445

Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp
    450             455             460

Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys
465             470             475             480

Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr
            485             490             495

His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr
            500             505             510

Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile
            515             520             525

Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu
            530             535             540

Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala
545             550             555             560

Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn
            565             570             575

Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr
            580             585             590

Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe
            595             600             605

Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn
        610             615             620

Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr
625             630             635             640
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Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650


<210>  53
<211>  1959
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin


<220>
<221>  CDS
<222>  (1)..(1956)

<400>  53
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct     48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat     96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg    144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat    192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta    240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt    288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca    336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt    384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat    432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt    480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
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aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt    528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                     170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc gga ttc gaa gtg    576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Gly Phe Glu Val
                180                     185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta    624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
                195                     200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa    672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                     215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac    720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                     230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga    768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                     250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa    816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                     265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat    864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
                275                     280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att    912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                     295                 300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca    960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                     310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat   1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                     330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt   1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340                     345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga   1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                355                     360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat   1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                     375                 380
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aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt        1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag        1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa        1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc        1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435             440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca        1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa        1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg        1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att        1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc        1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa        1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca        1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act        1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc        1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca        1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605
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ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag       1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc       1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                   1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650


<210>   54
<211>   652
<212>   PRT
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin

<400>   54

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Gly Phe Glu Val
```

```
            180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215             220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230             235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245                 250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295             300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310             315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325                 330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390             395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405                 410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470             475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
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Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210>  55
<211>  1956
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin


<220>
<221>  CDS
<222>  (1)..(1953)

<400>  55
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg     144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
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```
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat        192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta        240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt        288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

aac act ata tgg cca agt gaa gac cca tgg aag gct ttt atg gca caa        336
Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln
            100                 105                 110

gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt aaa        384
Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys
        115                 120                 125

gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat gtt        432
Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val
    130                 135                 140

aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga aat cca        480
Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn Pro
145                 150                 155                 160

cac agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt cat        528
His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
                165                 170                 175

ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg ctg        576
Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu
            180                 185                 190

ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta tta        624
Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu
            195                 200                 205

aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa gat        672
Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp
    210                 215                 220

gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac act        720
Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr
225                 230                 235                 240

gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga ggt        768
Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly
            245                 250                 255

tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa atg        816
Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met
            260                 265                 270
```

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act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat att        864
Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile
        275             280             285

cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att ttt        912
Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe
    290             295             300

acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca act        960
Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr
305             310             315             320

ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat tat       1008
Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr
            325             330             335

tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt ggg      1056
Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly
        340             345             350

aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga cct      1104
Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro
        355             360             365

agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat aaa      1152
Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys
370             375             380

tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt tat      1200
Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr
385             390             395             400

cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag gta      1248
Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val
            405             410             415

tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa aaa      1296
Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys
        420             425             430

aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc cat      1344
Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His
        435             440             445

gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca gat      1392
Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp
        450             455             460

gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa tgt      1440
Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys
465             470             475             480

ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg aca      1488
Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr
            485             490             495
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cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att act      1536
His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr
            500                 505                 510

caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc att      1584
Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile
            515                 520                 525

att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa gaa      1632
Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu
            530                 535                 540

tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca gcc      1680
Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala
545                 550                 555                 560

ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act aac      1728
Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn
                565                 570                 575

tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc tac      1776
Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr
            580                 585                 590

att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca ttt      1824
Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe
            595                 600                 605

gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag aat      1872
Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn
            610                 615                 620

gaa ctt ata ata gga gca gaa·tct ttc gtt tct aat gaa aaa atc tat      1920
Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr
625                 630                 635                 640

ata gat aag ata gaa ttt atc cca gta caa ttg taa                      1956
Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650


<210>   56
<211>   651
<212>   PRT
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin

<400>   56

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1                   5                   10                  15


Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35   40   45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50   55   60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85   90   95

Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln
            100   105   110

Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys
        115   120   125

Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val
    130   135   140

Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn Pro
145   150   155   160

His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
            165   170   175

Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu
            180   185   190

Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu
        195   200   205

Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp
    210   215   220

Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr
225   230   235   240

Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly
            245   250   255

Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met
            260   265   270

Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile
        275   280   285

Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe
    290   295   300

Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr
305   310   315   320

Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr
            325   330   335

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Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly
            340                 345             350

Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro
            355                 360             365

Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys
    370                 375                 380

Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr
385                 390                 395                 400

Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val
            405                 410                 415

Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys
            420                 425                 430

Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His
            435                 440                 445

Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp
    450                 455                 460

Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys
465                 470                 475                 480

Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr
            485                 490                 495

His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr
            500                 505                 510

Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile
            515                 520                 525

Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu
    530                 535                 540

Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala
545                 550                 555                 560

Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn
            565                 570                 575

Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr
            580                 585                 590

Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe
            595                 600                 605

Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn
            610                 615                 620

Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr
625                 630                 635                 640
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Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                  650


<210>  57
<211>  1956
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin


<220>
<221>  CDS
<222>  (1)..(1953)

<400>  57
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg     144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat     192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta     240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt     288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

aac act ata tgg cca agt gaa gac cca tgg aag gct ttt atg gca caa     336
Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln
            100                 105                 110

gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt aaa     384
Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys
        115                 120                 125

gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat gtt     432
Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val
        130                 135                 140

aat gcg tta aat tcc tgg aag aaa ttt cac cat tct cgt cgt tct aaa     480
Asn Ala Leu Asn Ser Trp Lys Lys Phe His His Ser Arg Arg Ser Lys
145                 150                 155                 160
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aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt cat        528
Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
                165             170             175

ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg ctg        576
Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu
                180             185             190

ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta tta        624
Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu
            195             200             205

aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa gat        672
Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp
        210             215             220

gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac act        720
Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr
225             230             235             240

gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga ggt        768
Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly
                245             250             255

tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa atg        816
Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met
            260             265             270

act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat att        864
Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile
            275             280             285

cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att ttt        912
Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe
        290             295             300

acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca act        960
Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr
305             310             315             320

ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat tat       1008
Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr
                325             330             335

tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt ggg       1056
Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly
                340             345             350

aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga cct       1104
Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro
                355             360             365

agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat aaa       1152
Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys
        370             375             380
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tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt tat          1200
Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr
385             390             395             400

cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag gta          1248
Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val
            405             410             415

tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa aaa          1296
Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys
            420             425             430

aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc cat          1344
Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His
            435             440             445

gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca gat          1392
Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp
            450             455             460

gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa tgt          1440
Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys
465             470             475             480

ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg aca          1488
Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr
                485             490             495

cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att act          1536
His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr
            500             505             510

caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc att          1584
Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile
            515             520             525

att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa gaa          1632
Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu
            530             535             540

tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca gcc          1680
Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala
545             550             555             560

ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act aac          1728
Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn
            565             570             575

tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc tac          1776
Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr
            580             585             590

att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca ttt          1824
Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe
            595             600             605

gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag aat          1872
Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn
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Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn
    610             615             620

gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc tat    1920
Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr
625             630             635             640

ata gat aag ata gaa ttt atc cca gta caa ttg taa    1956
Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645             650


<210>  58
<211>  651
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  58

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln
            100             105             110

Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys
            115             120             125

Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val
    130             135             140

Asn Ala Leu Asn Ser Trp Lys Lys Phe His His Ser Arg Arg Ser Lys
145             150             155             160

Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
            165             170             175

Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu
            180             185             190
```

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Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu
        195             200             205

Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp
    210             215             220

Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr
225             230             235             240

Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly
            245       ·     250             255

Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met
            260             265             270

Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile
        275             280             285

Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe
        290             295             300

Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr
305             310             315             320

Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr
            325             330             335

Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly
            340             345             350

Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro
            355             360             365

Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys
    370             375             380

Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr
385             390             395             400

Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val
            405             410             415

Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys
            420             425             430

Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His
            435             440             445

Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp
    450             455             460

Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys
465             470             475             480

Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr
            485             490             495
```

```
His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr
            500             505             510

Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile
            515             520             525

Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu
        530             535             540

Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala
545             550             555             560

Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn
            565             570             575

Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile Tyr
            580             585             590

Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe
            595             600             605

Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn
        610             615             620

Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile Tyr
625             630             635             640

Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650


<210>   59
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin


<220>
<221>   CDS
<222>   (1)..(1956)

<400>   59
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct       48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat       96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg      144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45
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act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat        192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta        240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt       288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca       336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt       384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat       432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt       480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

aaa aga agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt       528
Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg       576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta       624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195             200             205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa       672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac       720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga       768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa       816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270
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atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

ttt acg gat cca att ttt acc ctt aat aca cta cag aag tac gga cca        960
Phe Thr Asp Pro Ile Phe Thr Leu Asn Thr Leu Gln Lys Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat       1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt       1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga       1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat       1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt       1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag       1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa       1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc       1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca       1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa       1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg       1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att       1536
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Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530                 535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
            610                 615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650
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<210> 60
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 60

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
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Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50   55   60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85   90   95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100   105   110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
    115   120   125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130   135   140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165   170   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180   185   190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
    195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
    275   280   285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290   295   300

Phe Thr Asp Pro Ile Phe Thr Leu Asn Thr Leu Gln Lys Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405   410   415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435   440   445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450   455   460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465   470   475   480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485   490   495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500   505   510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515   520   525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530   535   540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545   550   555   560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565   570   575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580   585   590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595   600   605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610   615   620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625   630   635   640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu

<210> 61
<211> 1959
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 61
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct   48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat   96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20   25   30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35   40   45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat   192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50   55   60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85   90   95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca   336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100   105   110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt   384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115   120   125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat   432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130   135   140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt   480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

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aaa aga agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt       528
Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg       576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta       624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
                195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa       672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac       720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga       768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa       816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat       864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

gtt cgg tta tac cca aaa ggg gtt aaa aca gaa cta aca aga gac att       912
Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300

tct acg gat cca att ttt gcc gtt aat act ctg tgg gaa tac gga cca       960
Ser Thr Asp Pro Ile Phe Ala Val Asn Thr Leu Trp Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat      1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt cga cct ggt tac ttt      1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe
                340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gca gaa act aga      1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Ala Glu Thr Arg
        355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat      1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt      1200
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Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag    1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405             410             415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa    1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420             425             430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc    1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
                435             440             445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca    1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450             455             460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa    1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg    1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485             490             495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att    1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500             505             510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc    1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa    1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca    1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act    1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc    1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
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aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210> 62
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 62

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
        20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165             170             175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190
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Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210             215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230             235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275             280             285

Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

Ser Thr Asp Pro Ile Phe Ala Val Asn Thr Leu Trp Glu Tyr Gly Pro
305             310             315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe
        340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Ala Glu Thr Arg
        355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
        420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495
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```
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
            610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645             650
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<210> 63
<211> 1959
<212> DNA
<213> Artificial sequence
<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

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<400> 63
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct      48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat      96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg      144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35              40              45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat      192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60
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gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta        240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70                  75                  80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt        288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285
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gtt cgg tta tac cca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295                 300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat       1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt cga cct ggt tac ttt       1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe
            340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga       1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat       1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt       1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag       1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa       1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc       1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
    435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca       1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa       1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg       1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att       1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc       1584
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Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa    1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca    1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act    1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc    1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca    1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag    1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc    1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650


<210>  64
<211>  652
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin

<400>  64

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50              55              60
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Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165             170             175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
    195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
    275             280             285

Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe
            340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365
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Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650

<210>   65
<211>   1959
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<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1956)

<400> 65
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct   48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat   96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20   25   30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35   40   45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat   192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50   55   60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85   90   95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca   336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100   105   110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt   384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115   120   125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat   432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130   135   140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt   480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

aaa aga agc caa ggt cga ata agg gaa ctt ttt tct caa gca gaa agt   528
Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165   170   175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg   576

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His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta    624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa    672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac    720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga    768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa    816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat    864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att    912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

ttt acg gat cca att ttt tta ctt aat act ctt cag gag tat gga cca    960
Phe Thr Asp Pro Ile Phe Leu Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat   1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt   1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
                340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga   1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat   1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt   1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag   1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
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                405                      410                      415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa       1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                      425                  430          .

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc       1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435                      440                  445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca       1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450                      455                  460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa       1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                      470                  475                  480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg       1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                      490                  495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att       ·1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                      505                  510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc       1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                      520                  525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa       1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530                      535                  540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca       1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                      550                  555                  560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act       1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                      570                  575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc       1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580                      585                  590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca       1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595                      600                  605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag       1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
            610                      615                  620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc       1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                      630                  635                  640
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tat ata gat aag ata gaa ttt atc cca gta caa ttg taa          1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645           650
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<210> 66
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 66

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
            130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210             215             220
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Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
        260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275             280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290             295             300

Phe Thr Asp Pro Ile Phe Leu Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
        340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
        420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515             520             525
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Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610          ·    615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210>   67
<211>   1959
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Recombinant delta endotoxin

<220>
<221>   CDS
<222>   (1)..(1956)

<400>   67
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atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct       48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                   10                  15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat       96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                20                  25                  30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg      144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat      192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50                  55          ·        60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta      240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
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gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt        288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85                  90                  95

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100                 105                 110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115                 120                 125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130                 135                 140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260                 265                 270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275                 280                 285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290                 295                 300
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```
ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat       1008
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325                 330                 335

tat tta cag ggg att gaa ttt cat acg cgt ctt cga cct ggt tac ttt      1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe
                340                 345                 350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga      1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
                355                 360                 365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat      1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
                370                 375                 380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt      1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag      1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa      1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
                420                 425                 430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc      1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
                435                 440                 445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca      1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
                450                 455                 460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa      1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg      1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att      1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
                500                 505                 510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
                515                 520                 525
```

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att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565             570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
                580             585             590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
                595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645             650
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<210> 68
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 68

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80
```

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85   90   95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                100   105   110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115   120   125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130   135   140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165   170   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180   185   ' 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
    275   280   285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290   295   300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe
            340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370   375   380

```
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
    435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
    595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650

<210>   69
<211>   1482
<212>   DNA
<213>   Artificial sequence
<220>
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<223> Recombinant delta endotoxin

<220>
<221> CDS
<222> (1)..(1479)

<400> 69
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agt aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa          48
Ser Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu
1               5                   10                  15

agt cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa          96
Ser His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu
                20                  25                  30

gtg ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg         144
Val Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu
            35                  40                  45

cta tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca         192
Leu Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser
        50                  55                  60

gaa gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa         240
Glu Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln
65                  70                  75                  80

tac act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta         288
Tyr Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu
                85                  90                  95

aga ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga         336
Arg Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg
                100                 105                 110

gaa atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat         384
Glu Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr
            115                 120                 125

gat att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac         432
Asp Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp
        130                 135                 140

att ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga         480
Ile Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly
145                 150                 155                 160

cca act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt         528
Pro Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe
                165                 170                 175

gat tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac         576
Asp Tyr Leu Gln Gly Ile Glu Phe His Thr· Arg Leu Gln Pro Gly Tyr
                180                 185                 190

ttt ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act         624
Phe Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr
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```
aga cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga      672
Arg Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly
    210             215             220

gat aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa      720
Asp Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys
225             230             235             240

gtt tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt      768
Val Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly
                245             250             255

aag gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat      816
Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp
                260             265             270

caa aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat      864
Gln Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn
        275             280             285

ggc cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca      912
Gly His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr
    290             295             300

aca gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg      960
Thr Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala
305             310             315             320

gaa tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act     1008
Glu Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr
                325             330             335

tgg aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag     1056
Trp Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys
                340             345             350

att act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct     1104
Ile Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala
        355             360             365

tcc att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta     1152
Ser Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu
    370             375             380

aaa gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca     1200
Lys Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser
385             390             395             400

gca gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc     1248
Ala Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr
        405             410             415

act aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc     1296
Thr Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val
        420             425             430
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atc tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa        1344
Ile Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln
        435             440             445

aca ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat        1392
Thr Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp
    450             455             460

aag aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa        1440
Lys Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys
465             470             475             480

atc tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                1482
Ile Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            485             490
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<210> 70
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 70

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Ser Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu
1               5               10              15

Ser His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu
                20              25              30

Val Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu
        35              40              45

Leu Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser
    50              55              60

Glu Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln
65              70              75              80

Tyr Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu
                85              90              95

Arg Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg
            100             105             110

Glu Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr
        115             120             125

Asp Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp
    130             135             140

Ile Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly
145             150             155             160
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Pro Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe
              165   170   175

Asp Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr
              180   185   190

Phe Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr
              195   200   205

Arg Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly
    ·210   215   220

Asp Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys
225   230   235   240

Val Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly
              245   250   255

Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp
              260   265   270

Gln Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn
              275   280   285

Gly His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr
    290   295   300

Thr Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala
305   310   315   320

Glu Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr
              325   330   335

Trp Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys
              340   345   350

Ile Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala
              355   360   365

Ser Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu
    370   375   380

Lys Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser
385   390   395   400

Ala Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr
              405   410   415

Thr Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val
              420   425   430

Ile Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln
              435   440   445

Thr Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp
    450   455   460

```
Lys Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys
465                 470                 475                 480

Ile Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                485                 490
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<210> 71
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Oligonucleotide

<400> 71
agacaactct acagtaaaag atg   23

<210> 72
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Oligonucleotide

<400> 72
ggtaattggt caatagaatc   20

<210> 73
<211> 39
<212> DNA
<213> Artificial sequence

<220>
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<220>
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<222> (21)..(23)
<223> N = A, T, G, C (25% each)

<400> 73
cagaagatgt tgctgaattc nnncatagac aattaaaac   39

<210> 74
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Oligonucleotide

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<223>  N = A, T, G, C (25% each)

<400>  74
gatgttgctg aattctatnn nagacaatta aaac                              34


<210>  75
<211>  33
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide


<220>
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<223>  N = A, T, C (16% each); G (52%)

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<222>  (18)..(18)
<223>  N = T, G, C (10% each); A (70%)

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<222>  (19)..(19)
<223>  N = A, T, G, C (25% each)

<400>  75
cccattttat gatattnnnt tatactcaaa agg                              33


<210>  76
<211>  64
<212>  DNA
<213>  Artificial sequence

<220>
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<220>
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<222>  (24)..(24)
<223>  N = T, G, C (6% each); A (82%)

<220>
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<222>  (25)..(25)
<223>  N = A, T, G (6% each); C (82%)
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<220>
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<223>  N = A, T, G, C (25% each)


<220>
<221>  misc_feature
<222>  (27)..(28)
<223>  N = A, T, G (6%) each); C (82%)


<220>
<221>  misc_feature
<222>  (29)..(29)
<223>  N = A, T, G, C (25% each)


<220>
<221>  misc_feature
<222>  (30)..(30)
<223>  N = A, T, G (6% each); C (82%)


<220>
<221>  misc_feature
<222>  (31)..(31)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (32)..(32)
<223>  N = A, T, G, C (25%)


<220>
<221>  .misc_feature
<222>  (33)..(33)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (34)..(34)
<223>  N = A, T, G (6% each) ; C (82%)


<220>
<221>  misc_feature
<222>  (35)..(35)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (36)..(36)
<223>  N = A, T, G (6% each) ; C (82%)


<220>
<221>  misc_feature
<222>  (37)..(37)
<223>  N = A, G, C (6% each); T (82%)


<220>
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<221>  misc_feature
<222>  (38)..(38)
<223>  N = A, T, G, C (25% each)

<220>
<221>  misc_feature
<222>  (39)..(39)
<223>  N = A, T, G (6% each); C  (82%)

<220>
<221>  misc_feature
<222>  (40)..(40)
<223>  N = A, T, C (6% each); G (82%)

<220>
<221>  misc_feature
<222>  (41)..(41)
<223>  N = A, T, G, C (25% each)

<220>
<221>  misc_feature
<222>  (42)..(42)
<223>  N = A, G, C (6% each); T (82%)

<220>
<221>  misc_feature
<222>  (43)..(43)
<223>  N = A, T, G (6% each); C (82%)

<220>
<221>  misc_feature
<222>  (44)..(44)
<223>  N = A, G, C (6% each); T (82%)

<400>  76
agctatgctg gtctcggaag aaannnnnnn nnnnnnnnnn nnnnaaaaga agccaagatc      60

gaat                                                                  64


<210>  77
<211>  40
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  77
ggtcacctag gtctctcttc caggaattta acgcattaac                           40


<210>  78
<211>  65
<212>  DNA
<213>  Artificial sequence
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<220>
<223>  Synthetic Oligonucleotide


<220>
<221>  misc_feature
<222>  (22)..(22)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (23)..(23)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (24)..(24)
<223>  N = A, T, G (1% each); C (97%)


<220>
<221>  misc_feature
<222>  (25)..(25)
<223>  N = A, T, C (6% each); G (82%)


<220>
<221>  misc_feature
<222>  (26)..(26)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (28)..(28)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (29)..(29)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (30)..(30)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (31)..(31)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (32)..(33)
```

```
<223>  N = A, T, C (6% each); G (82%)

<220>
<221>  misc_feature
<222>  (34)..(34)
<223>  N = A, T, G (15% each); C (55%)

<220>
<221>  misc_feature
<222>  (35)..(36)
<223>  N = A, G, C (15% each); T (55%)

<220>
<221>  misc_feature
<222>  (37)..(37)
<223>  N = A, G, C (6% each); T (82%)

<220>
<221>  misc_feature
<222>  (38)..(38)
<223>  N = T, G, C (6% each); A (82%)

<220>
<221>  misc_feature
<222>  (39)..(39)
<223>  N = A, T, G (1% each); C (97%)

<220>
<221>  misc_feature
<222>  (40)..(40)
<223>  N = T, G, C (6% each); A (82%)

<220>
<221>  misc_feature
<222>  (41)..(41)
<223>  N = A, T, C (6% each); G (82%)

<220>
<221>  misc_feature
<222>  (42)..(42)
<223>  N = A, G, C (6% each); T (82%)

<220>
<221>  misc_feature
<222>  (43)..(44)
<223>  N = T, G, C (6% each); A (82%)

<220>
<221>  misc_feature
<222>  (45)..(45)
<223>  N = A, T, G, C (25% each)

<220>
<221>  misc_feature
<222>  (46)..(48)
<223>  N = A, T, C (6% each); G (82%)
```

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<400>  78
agctatgctg gtctcccatt tnnnnnnnnn nnnnnnnnnn nnnnnnnngt taaaacagaa      60

ctaac                                                                  65


<210>  79
<211>  36
<212>  DNA
<213>  Artificial sequence

<220>    .
<223>  Synthetic Oligonucleotide

<400>  79
atccagtggg gtctcaaatg ggaaaagtac aattag                                36


<210>  80
<211>  63
<212>  DNA
<213>  Artificial sequence

<220>              .
<223>  Synthetic Oligonucleotide


<220>
<221>  misc_feature
<222>  (23)..(23)
<223>  N = A, G, C (6% each); T (82%)

<220>
<221>  misc_feature
<222>  (24)..(26)
<223>  N = A, T, G (6% each); C (82%)

<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  N = A, G, C (6% each); T (82%)

<220>
<221>  misc_feature
<222>  (28)..(28)
<223>  N = A, T, G (6% each); C (82%)

<220>
<221>  misc_feature
<222>  (29)..(30)
<223>  N = T, G, C (6% each); A (82%)

<220>
<221>  misc_feature
<222>  (31)..(31)
<223>  N = A, G, C (6% each); T (82%)
```

```
<220>
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<222> (32)..(32)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (33)..(33)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (34)..(34)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (35)..(35)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (36)..(36)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (37)..(37)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (38)..(38)
<223> N = A, T, G (6% each); C (82%)

<220>
<221> misc_feature
<222> (39)..(39)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (40)..(40)
<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (41)..(41)
<223> N = A, C (8% each); T (1%); G (83%)

<220>
<221> misc_feature
<222> (42)..(42)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
```

```
<222>  (43)..(43)
<223>  N = A, T, C (6% each); G (82%)


<220>
<221>  misc_feature
<222>  (44)..(44)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (45)..(45)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (46)..(46)
<223>  N = A, T,G (1% each); C (97%)


<400>  80
catttttacg gatccaattt ttnnnnnnnn nnnnnnnnnn nnnnnnggac caactttttt        60

gag                                                                     63


<210>  81
<211>  62
<212>  DNA
<213>  Artificial sequence


<220>
<223>  Synthetic Oligonucleotide



<220>
<221>  misc_feature
<222>  (28)..(28)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (29)..(29)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (30)..(30)
<223>  N = A, T, G (1% each); C (97%)


<220>
<221>  misc_feature
<222>  (31)..(33)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (34)..(35)
<223>  N = A, T, C (6% each); G (82%)
```

```
<220>
<221> misc_feature
<222> (36)..(36)
<223> N = A, T, G, C (25% each)

<220>
<221> misc_feature
<222> (37)..(37)
<223> N = A (82%); T (2%); G, C (8% each)

<220>
<221> misc_feature
<222> (38)..(39)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (40)..(40)
<223> N = A, T, C (6% each); G (82%)

<220>
<221> misc_feature
<222> (41)..(41)
<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (42)..(42)
<223> N = A, G, C (6% each); T (82%)

<400>  81
gaatttcata cgcgtcttca acctggtnnn nnnnnnnnn nntctttcaa ttattggtct        60

gg                                                                      62


<210>  82
<211>  73
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide


<220>
<221> misc_feature
<222> (41)..(41)
<223> N = A, G, C (6% each); T (82%)

<220>
<221> misc_feature
<222> (42)..(43)
<223> N = A (0%); T,C (9% each); G (82%)

<220>
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<221>  misc_feature
<222>  (44)..(45)
<223>  N = A, T, G (6% each); C (82%)


<220>
<221>  misc_feature
<222>  (46)..(46)
<223>  N = A, T, G, C (25% each)


<220>
<221>  misc_feature
<222>  (47)..(48)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (49)..(49)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (50)..(51)
<223>  N = A, T, C (6% each); G (82%)


<220>
<221>  misc_feature
<222>  (52)..(52)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (53)..(54)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (55)..(55)
<223>  N = A, T, C (6% each); G (82%)


<400>  82
aaaagtttat cgaactatag ctaatacaga cgtagcggct nnnnnnnnnn nnnnngtata      60

tttaggtgtt acg                                                         73



<210>  83
<211>  20
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  83
ggagttccat ttgctggggc                                                  20
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<210>  84
<211>  17
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  84
atctccataa aatgggg                                                    17


<210>  85
<211>  32
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  85
gcgaagtaaa agaagccaag gtcgaataag gg                                   32


<210>  86
<211>  43
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  86
cctttaagtt tgcgaaatcc acacagccaa ggtcgaataa ggg                       43


<210>  87
<211>  35
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  87
cccattttat gatgttcggt tatacccaaa agggg                                35


<210>  88
<211>  25
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  88
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ggccaagtga agacccatgg aaggc                                                25


<210>  89
<211>  22
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  89
gcagtttccg gattcgaagt gc                                                    22

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<210>  90
<211>  17
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  90
ccgctacgtc tgtatta                                                         17


<210>  91
<211>  17
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  91
ataatggaag cacctga                                                         17


<210>  92
<211>  60
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide


<220>
<221>  misc_feature
<222>  (22)..(22)
<223>  N = T, G, C (6% each); A (82%)

<220>
<221>  misc_feature
<222>  (23)..(23)
<223>  N = A, G, C (6% each); T (82%)
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<220>
<221>  misc_feature
<222>  (24)..(24)
<223>  N = A, T, C (6% each); G (82%)


<220>
<221>  misc_feature
<222>  (25)..(25)
<223>  N = A, T, G (6% each); C (82%)


<220>
<221>  misc_feature
<222>  (26)..(26)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (27)..(28)
<223>  N = A, T, C (6% each); G (82%)


<220>
<221>  misc_feature
<222>  (29)..(29)
<223>  N = T, G, C (6% each); A (82%)


<220>
<221>  misc_feature
<222>  (30)..(31)
<223>  N = A, T, G (6% each); C (82%)


<220>
<221>  misc_feature
<222>  (32)..(32)
<223>  N = A, T, C (6% each); G (82%)


<220>
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<222>  (33)..(33)
<223>  N = A, G, C (6% each); T (82%)


<220>
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<222>  (34)..(34)
<223>  N = A, T, G (6% each); C (82%)


<220>
<221>  misc_feature
<222>  (35)..(35)
<223>  N = A, T, C (6% each); G (82%)


<220>
<221>  misc_feature
<222>  (36)..(36)
<223>  N = A, G, C (6% each); T (82%)


<220>
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<221>  misc_feature
<222>  (37)..(38)
<223>  N = A, T, C (6% each); G (82%)

<220>
<221>  misc_feature
<222>  (39)..(39)
<223>  N = A, T, G, C (25% each)

<400>  92
agctatgctg gtctcttctt annnnnnnnn nnnnnnnnna caattccatt ttttacttgg      60


<210>  93
<211>  40
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  93
atccagttgg gtctctaaga aacaaaccgc gtaattaagc                            40


<210>  94
<211>  20
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide

<400>  94
cctcaagggt tataacatcc                                                  20


<210>  95
<211>  55
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic Oligonucleotide


<220>
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<222>  (19)..(19)
<223>  N = A, T, C (6% each); G (82%)

<220>
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<222>  (20)..(20)
<223>  N = T, G, C (6% each); A (82%)

<220>
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<221>  misc_feature
<222>  (21)..(21)
<223>  N = A, G, C (6% each); T (82%)


<220>
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<222>  (22)..(23)
<223>  N = A, T, C (6% each); G (82%)


<220>
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<222>  (24)..(24)
<223>  N = A, T, G, C (25% each)


<220>
<221>  misc_feature
<222>  (25)..(25)
<223>  N = A, G (8% each); T (2%); C (82%)


<220>
<221>  misc_feature
<222>  (26)..(27)
<223>  N = T, G, C (6% each); A (82%)


<220>
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<222>  (28)..(28)
<223>  N = A (82%); T (2%); G,C (8% each)


<220>
<221>  misc_feature
<222>  (29)..(30)
<223>  N = T, G, C (6% each); A (82%)


<220>
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<222>  (31)..(31)
<223>  N = A, T, C (6% each); G (82%)


<220>
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<222>  (32)..(32)
<223>  N = A, G, C (6% each); T (82%)


<220>
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<222>  (33)..(33)
<223>  N = A, T, G, C (25% each)


<220>
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<222>  (34)..(34)
<223>  N = A, G, C (6% each); T (82%)


<220>
<221>  misc_feature
<222>  (35)..(35)
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<223> N = T, G, C (6% each); A (82%)

<220>
<221> misc_feature
<222> (36)..(36)
<223> N = A, G, C (1% each); T (97%)

<400> 95
gtacaaaagc taagctttnn nnnnnnnnnn nnnnnncgaa ctatagctaa tacag   55

<210> 96
<211> 7
<212> PRT
<213> Bacillus thuringiensis

<400> 96

Ser Lys Arg Ser Gln Asp Arg
1   5

<210> 97
<211> 1959
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)..(1956)

<400> 97
atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct   48
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1   5   10   15

aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat   96
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20   25   30

cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg   144
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35   40   45

act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat   192
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50   55   60

gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta   240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65   70   75   80

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt   288
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85   90   95

```
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca        336
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt        384
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115             120             125

aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat        432
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
            130             135             140

gtt aat gcg tta aat tcc tgg aag aaa aca cct tta agt ttg cga agt        480
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155             160

aaa aga agc caa gat cga ata agg gaa ctt ttt tct caa gca gaa agt        528
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165             170             175   .

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg        576
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta        624
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca gaa        672
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
            210             215             220

gat gtt gct gaa ttt tat cat aga caa tta aaa ctt aca caa caa tac        720
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235             240

act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta aga        768
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245             250             255

ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga gaa        816
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
                260             265             270

atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat gat        864
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac att        912
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
            290             295             300

ttt acg gat cca att ttt tca ctt aat act ctt cag gag tat gga cca        960
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt gat      1008
```

```
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
                325              330              335

tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac ttt      1056
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340              345              350

ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act aga      1104
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355              360              365

cct agt ata gga tct agt aag aca att act tcc cca ttt tat gga gat      1152
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
            370              375              380

aaa tct act gaa cct gta caa aag cta agc ttt gat gga caa aaa gtt      1200
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385              390              395              400

tat cga act ata gct aat aca gac gta gcg gct tgg ccg aat ggt aag      1248
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405              410              415

gta tat tta ggt gtt acg aaa gtt gat ttt agt caa tat gat gat caa      1296
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420              425              430

aaa aat gaa act agt aca caa aca tat gat tca aaa aga aac aat ggc      1344
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435              440              445

cat gta agt gca cag gat tct att gac caa tta ccg cca gaa aca aca      1392
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
            450              455              460

gat gaa cca ctt gaa aaa gca tat agt cat cag ctt aat tac gcg gaa      1440
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465              470              475              480

tgt ttc tta atg cag gac cgt cgt gga aca att cca ttt ttt act tgg      1488
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485              490              495

aca cat aga agt gta gac ttt ttt aat aca att gat gct gaa aag att      1536
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500              505              510

act caa ctt cca gta gtg aaa gca tat gcc ttg tct tca ggt gct tcc      1584
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515              520              525

att att gaa ggt cca gga ttc aca gga gga aat tta cta ttc cta aaa      1632
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530              535              540

gaa tct agt aat tca att gct aaa ttt aaa gtt aca tta aat tca gca      1680
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
```

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gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act      1728
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565                 570             575

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc      1776
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580             585                 590

tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca      1824
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595             600             605

ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag      1872
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610             615             620

aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc      1920
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630      •          635                 640

tat ata gat aag ata gaa ttt atc cca gta caa ttg taa                  1959
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650
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<210> 98
<211> 652
<212> PRT
<213> Bacillus thuringiensis

<400> 98

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1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115             120             125
```

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Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130                 135                 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145                 150                 155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                165                 170                 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                180                 185                 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195                 200                 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210                 215                 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225                 230                 235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
                245                 250                 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260                 265                 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275                 280                 285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290                 295                 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305                 310                 315                 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325                 330                 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
        340                 345                 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355                 360                 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370                 375                 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385                 390                 395                 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
                405                 410                 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430
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```
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435                 440                 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
        450                 455                 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
                485                 490                 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500                 505                 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515                 520                 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
        530                 535                 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
        580                 585                 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
        610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650
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<210> 99
<211> 2000
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 99
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gaggaactta actacaagga gtttctccgg atgaccgaag atagctccac tgaggttctc   180

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gataactcta cagtgaagga cgctgttgga actggcatta gcgttgtggg acagattctt    240

ggagtggttg gtgttccatt cgctggagct ttgaccagct tctaccagtc ctttctcaac    300

accatctggc cttcagatgc tgatccctgg aaggctttca tggcccaagt ggaagtcttg    360

atcgataaga agatcgaaga gtatgccaag tctaaagcct tggctgagtt gcaaggtttg    420

cagaacaact tcgaggatta cgtcaacgca ctcaacagct ggaagaaaac tcccttgagt    480

ctcaggtcta agcgttccca ggaccgtatt cgtgaacttt tcagccaagc cgaatcccac    540

ttcagaaact ccatgcctag ctttgccgtt tctaagttcg aggtgctctt cttgccaaca    600

tacgcacaag ctgccaacac tcatctcttg cttctcaaag acgctcaggt gtttggtgag    660

gaatggggtt actccagtga agatgttgcc gagttctacc gtaggcagct caagttgact    720

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tctacctacg acgcatgggt gaagttcaac aggtttcgta gagagatgac cttgactgtg    840

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tacggtccaa cttttctctc cattgagaac agcatcagga agcctcacct cttcgactat   1020

ctgcaaggca ttgagtttca caccaggttg caacctggtt acttcggtaa ggattccttc   1080

aactactgga gcggaaacta cgttgaaacc agaccatcca tcggatctag caagaccatc   1140

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cagaaggtgt atagaaccat cgccaatacc gatgttgcag cttggcctaa tggcaaggtc   1260

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caacttccac ctgaaaccac tgatgaacca ttggagaagg cttacagtca ccaacttaac   1440

tacgccgaat gctttctcat gcaagacagg cgtggcacca ttccgttctt tacatggact   1500

cacaggtctg tcgacttctt taacactatc gacgctgaga agattaccca acttcccgtg   1560

gtcaaggctt atgccttgtc cagcggagct tccatcattg aaggtccagg cttcaccggt   1620

ggcaacttgc tcttccttaa ggagtccagc aactccatcg ccaagttcaa agtgacactt   1680

aactcagcag ccttgctcca acgttacagg gttcgtatca gatacgcaag cactaccaat   1740

cttcgcctct tgtccagaa cagcaacaat gatttccttg tcatctacat caacaagact   1800

atgaacaaag acgatgacct cacctaccaa acattcgatc ttgccactac caatagtaac   1860
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atgggattct ctggtgacaa gaacgagctg atcataggtg ctgagagctt tgtctctaat   1920

gagaagattt acatagacaa gatcgagttc attccagttc aactctaata gatcccccgg   1980

gctgcaggaa ttcgatatca   2000

<210> 100
<211> 653
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 100

Met Ala Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr
1   5   10   15

Pro Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp
            20   25   30

Asn Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg
        35   40   45

Met Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys
    50   55   60

Asp Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val
65   70   75   80

Val Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe
                85   90   95

Leu Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met
            100   105   110

Ala Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys
        115   120   125

Ser Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp
    130   135   140

Tyr Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg
145   150   155   160

Ser Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu
                165   170   175

Ser His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu
                180   185   190

Val Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu
        195   200   205

Leu Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser

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        210                    215                    220

Glu Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln
225                 230                 235                 240

Tyr Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu
                245                 250                 255

Arg Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg
            260                 265                 270

Glu Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr
        275                 280                 285

Asp Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp
    290                 295                 300

Ile Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly
305                 310                 315                 320

Pro Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe
            325                 330                 335

Asp Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr
        340                 345                 350

Phe Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr
        355                 360                 365

Arg Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly
    370                 375                 380

Asp Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys
385                 390                 395                 400

Val Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly
            405                 410                 415

Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp
        420                 425                 430

Gln Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn
    435                 440                 445

Gly His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr
    450                 455                 460

Thr Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala
465                 470                 475                 480

Glu Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr
            485                 490                 495

Trp Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys
        500                 505                 510

Ile Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala
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Ser Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu
    530   535   540

Lys Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser
545   550   555   560

Ala Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr
            565   570   575

Thr Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val
        580   585   590

Ile Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln
    595   600   605

Thr Phe Asp Leu Ala· Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp
    610   615   620

Lys Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys
625   630   635   640

Ile Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645   650

<210>   101
<211>   2050
<212>   DNA
<213>   Bacillus thuringiensis

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aatcacaacc agtacccatt ggctgacaat cctaacagta ctcttgagga acttaactac   180

aaggagtttc tccggatgac cgaagatagc tccactgagg ttctcgataa ctctacagtg   240

aaggacgctg ttggaactgg cattagcgtt gtgggacaga ttcttggagt ggttggtgtt   300

ccattcgctg agctttgac cagcttctac cagtcctttc tcaacaccat ctggccttca   360

gatgctgatc cctggaaggc tttcatggcc caagtggaag tcttgatcga taagaagatc   420

gaagagtatg ccaagtctaa agccttggct gagttgcaag gtttgcagaa caacttcgag   480

gattacgtca cgcactcaa cagctggaag aaaactccct tgagtctcag gtctaagcgt   540

tcccaggacc gtattcgtga acttttcagc caagccgaat cccacttcag aaactccatg   600

cctagctttg ccgtttctaa gttcgaggtg ctcttcttgc caacatacgc acaagctgcc   660

H: 532973(BF8T011.DOC)   217

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agtgaagatg ttgccgagtt ctaccatagg cagctcaagt tgactcaaca gtacacagac       780

cactgcgtca actggtacaa cgttgggctc aatggtctta gaggatctac ctacgacgca       840

tgggtgaagt tcaacaggtt tcgtagagag atgaccttga ctgtgctcga tcttatcgtt       900

ctctttccat tctacgacat tcgtctttac tccaaaggcg ttaagacaga gctgaccaga       960

gacatcttca ccgatcccat cttctcactt aacaccctgc aggaatacgg tccaactttt      1020

ctctccattg agaacagcat caggaagcct cacctcttcg actatctgca aggcattgag      1080

tttcacacca ggttgcaacc tggttacttc ggtaaggatt ccttcaacta ctggagcgga      1140

aactacgttg aaaccagacc atccatcgga tctagcaaga ccatcacttc tccattctac      1200

ggtgacaaga gcactgagcc agtgcagaag ttgagcttcg atgggcagaa ggtgtataga      1260

accatcgcca ataccgatgt tgcagcttgg cctaatggca aggtctacct tggagttact      1320

aaagtggact ctcccaata cgacgatcag aagaacgaga catctactca aacctacgat      1380

agtaagagga acaatggcca tgtttccgca caagactcca ttgaccaact tccacctgaa      1440

accactgatg aaccattgga gaaggcttac agtcaccaac ttaactacgc cgaatgcttt      1500

ctcatgcaag acaggcgtgg caccattccg ttctttacat ggactcacag gtctgtcgac      1560

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gacaagaacg agctgatcat aggtgctgag agctttgtct ctaatgagaa gatttacata      1980

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<210>   102
<211>   2280
<212>   DNA
<213>   Bacillus thuringiensis

<400>   102
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ttataatgtt caatagtttt atgggaaggc attttatcag gtagaaagtt atgtattatg    180

ataagaatgg gaggaagaaa aatgaatcca aacaatcgaa gtgaacatga tacgataaag    240

gttacaccta acagtgaatt gcaaactaac cataatcaat atcctttagc tgacaatcca    300

aattcaacac tagaagaatt aaattataaa gaattttaa gaatgactga agacagttct    360

acggaagtgc tagacaactc tacagtaaaa gatgcagttg ggacaggaat ttctgttgta    420

gggcagattt taggtgttgt aggagttcca tttgctgggg cactcacttc attttatcaa    480

tcatttctta acactatatg gccaagtgat gctgacccat ggaaggcttt tatggcacaa    540

gttgaagtac tgatagataa gaaaatagag gagtatgcta aaagtaaagc tcttgcagag    600

ttacagggtc ttcaaaataa tttcgaagat tatgttaatg cgttaaattc ctggaagaaa    660

acacctttaa gtttgcgaag taaaagaagc caagatcgaa taagggaact tttttctcaa    720

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gtttttggag aagaatgggg atattcttca gaagatgttg ctgaatttta tcatagacaa    900

ttaaaactta cacaacaata cactgaccat tgtgttaatt ggtataatgt tggattaaat    960

ggtttaagag gttcaactta tgatgcatgg gtcaaattta accgttttcg cagagaaatg   1020

actttaactg tattagatct aattgtactt ttcccatttt atgatattcg gttatactca   1080

aaagggttta aaacagaact aacaagagac attttttacgg atccaatttt ttcacttaat   1140

actcttcagg agtatggacc aactttttg agtatagaaa actctattcg aaaacctcat   1200

ttatttgatt atttacaggg gattgaattt catacgcgtc ttcaacctgg ttactttggg   1260

aaagattctt tcaattattg gtctggtaat tatgtagaaa ctagacctag tataggatct   1320

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aatgaaacta gtacacaaac atatgattca aaaagaaaca atggccatgt aagtgcacag   1560

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catcagctta attacgcgga atgtttctta atgcaggacc gtcgtggaac aattccattt   1680

tttacttgga cacatagaag tgtagacttt tttaatacaa ttgatgctga aaagattact   1740
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caacttccag tagtgaaagc atatgccttg tcttcaggtg cttccattat tgaaggtcca   1800

ggattcacag gaggaaattt actattccta aaagaatcta gtaattcaat tgctaaattt   1860

aaagttacat taaattcagc agccttgtta caacgatatc gtgtaagaat acgctatgct   1920

tctaccacta acttacgact ttttgtgcaa aattcaaaca atgattttct tgtcatctac   1980

attaataaaa ctatgaataa agatgatgat ttaacatatc aaacatttga tctcgcaact   2040

actaattcta atatggggtt ctcgggtgat aagaatgaac ttataatagg agcagaatct   2100

ttcgtttcta atgaaaaaat ctatatagat aagatagaat ttatcccagt acaattgtaa   2160

ggagatttta aaatgttggg tgatggtcaa aatgaaagaa taggaaggtg aattttgatg   2220

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<210> 103
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Oligonucleotide

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<212> DNA
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<220>
<223> Synthetic Oligonucleotide

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<210> 105
<211> 28
<212> DNA
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<220>
<223> Synthetic Oligonucleotide

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<210> 106
<211> 25

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<212>  DNA
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<220>
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<210>  107
<211>  1959
<212>  DNA
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<220>
<223>  Recombinant delta endotoxin

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aattataaag aatttttaag aatgactgaa gacagttcta cggaagtgct agacaactct     180

acagtaaaag atgcagttgg gacaggaatt tctgttgtag ggcagatttt aggtgttgta     240

ggagttccat ttgctggggc actcacttca ttttatcaat catttcttaa cactatatgg     300

ccaagtgatg ctgacccatg gaaggctttt atggcacaag ttgaagtact gatagataag     360

aaaatagagg agtatgctaa aagtaaagct cttgcagagt tacagggtct tcaaaataat     420

ttcgaagatt atgttaatgc gttaaattcc tggaagaaaa cacctttaag tttgcgaagt     480

aaaagaagcc aaggtcgaat aagggaactt ttttctcaag cagaaagtca ttttcgtaat     540

tccatgccgt catttgcagt ttccaaattc gaagtgctgt ttctaccaac atatgcacaa     600

gctgcaaata cacatttatt gctattaaaa gatgctcaag tttttggaga gaatggggga     660

tattcttcag aagatgttgc tgaattctat cgtagacaat aaaacttac acaacaatac      720

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gatgcatggg tcaaatttaa ccgttttcgc agagaaatga ctttaactgt attagatcta     840

attgtacttt tcccatttta tgatattcgg ttatactcaa aagggggttaa aacagaacta     900

acaagagaca tttttacgga tccaattttt ttacttacta cgcttcagaa gtacggacca     960

actttttga gtatagaaaa ctctattcga aaacctcatt tatttgatta tttacagggg     1020

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tctggtaatt atgtagaaac tagacctagt ataggatcta gtaagacaat tacttcccca     1140
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tatcgaacta tagctaatac agacgtagcg gcttggccga atggtaaggt atatttaggt   1260

gttacgaaag ttgattttag tcaatatgat gatcaaaaaa atgaaactag tacacaaaca   1320

tatgattcaa aaagaaacaa tggccatgta agtgcacagg attctattga ccaattaccg   1380

ccagaaacaa cagatgaacc acttgaaaaa gcatatagtc atcagcttaa ttacgcggaa   1440

tgtttcttaa tgcaggaccg tcgtggaaca attccatttt ttacttggac acatagaagt   1500

gtagactttt ttaatacaat tgatgctgaa aagattactc aacttccagt agtgaaagca   1560

tatgccttgt cttcaggtgc ttccattatt gaaggtccag gattcacagg aggaaattta   1620

ctattcctaa aagaatctag taattcaatt gctaaattta aagttacatt aaattcagca   1680

gccttgttac aacgatatcg tgtaagaata cgctatgctt ctaccactaa cttacgactt   1740

tttgtgcaaa attcaaacaa tgattttctt gtcatctaca ttaataaaac tatgaataaa   1800

gatgatgatt aacatatca aacatttgat ctcgcaacta ctaattctaa tatggggttc   1860

tcgggtgata agaatgaact tataatagga gcagaatctt tcgtttctaa tgaaaaaatc   1920

tatatagata agatagaatt tatcccagta caattgtaa                         1959
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<210> 108
<211> 652
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 108

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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5                  10                  15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20                  25                  30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35                  40                  45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50                  55                  60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65                  70                  75                  80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                85                  90                  95
```

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
        100   105   110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
        115   120   125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
        130   135   140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145   150   155   160

Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165   170   175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180   185   190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210   215   220

Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275   280   285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
        290   295   300

Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
        370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

```
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405                 410                 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
            420                 425                 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
            435                 440                 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450                 455                 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465                 470                 475                 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485                 490                 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505                · 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
            515                 520                 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
            530                 535                 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565                 570                 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
            595                 600                 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645                 650
```

<210> 109
<211> 649
<212> PRT
<213> Artificial sequence

<220>
<223> Recombinant delta endotoxin

<400> 109

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Ala Thr Glu
1   5   10   15

Asn Asn Glu Val Ser Asn Asn His Ala Gln Tyr Pro Leu Ala Asp Thr
            20   25   30

Pro Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Arg Thr Thr
        35   40   45

Asp Asn Asn Val Glu Ala Leu Asp Ser Ser Thr Thr Lys Asp Ala Ile
    50   55   60

Gln Lys Gly Ile Ser Ile Ile Gly Asp Leu Leu Gly Val Val Gly Phe
65   70   75   80

Pro Tyr Gly Gly Ala Leu Val Ser Phe Tyr Thr Asn Leu Leu Asn Thr
            85   90   95

Ile Trp Pro Gly Glu Asp Pro Leu Lys Ala Phe Met Gln Gln Val Glu
        100   105   110

Ala Leu Ile Asp Gln Lys Ile Ala Asp Tyr Ala Lys Asp Lys Ala Thr
        115   120   125

Ala Glu Leu Gln Gly Leu Lys Asn Val Phe Lys Asp Tyr Val Ser Ala
    130   135   140

Leu Asp Ser Trp Asp Lys Thr Pro Leu Thr Leu Arg Asp Gly Arg Ser
145   150   155   160

Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His Phe Arg
            165   170   175

Arg Ser Met Pro Ser Phe Ala Val Ser Gly Tyr Glu Val Leu Phe Leu
            180   185   190

Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Leu Lys Asp
        195   200   205

Ala Gln Ile Tyr Gly Thr Asp Trp Gly Tyr Ser Thr Asp Asp Leu Asn
    210   215   220

Glu Phe His Thr Lys Gln Lys Asp Leu Thr Ile Glu Tyr Thr Asn His
225   230   235   240

Cys Ala Lys Trp Tyr Lys Ala Gly Leu Asp Lys Leu Arg Gly Ser Thr
            245   250   255

Tyr Glu Glu Trp Val Lys Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu
            260   265   270

Thr Val Leu Asp Leu Ile Thr Leu Phe Pro Leu Tyr Asp Val Arg Thr
    275   280   285

Tyr Thr Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Val Leu Thr Asp

Pro Ile Val Ala Val Asn Asn Met Asn Gly Tyr Gly Thr Thr Phe Ser
305   310   315   320

Asn Ile Glu Asn Tyr Ile Arg Lys Pro His Leu Phe Asp Tyr Leu His
               325   330   335

Ala Ile Gln Phe His Ser Arg Leu Gln Pro Gly Tyr Phe Gly Thr Asp
               340   345   350

Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Ser Thr Arg Ser Ser Ile
               355   360   365

Gly Ser Asp Glu Ile Ile Arg Ser Pro Phe Tyr Gly Asn Lys Ser Thr
       370   375   380

Leu Asp Val Gln Asn Leu Glu Phe Asn Gly Glu Lys Val Phe Arg Ala
385   390   395   400

Val Ala Asn Gly Asn Leu Ala Val Trp Pro Val Gly Thr Gly Gly Thr
               405   410   415

Lys Ile His Ser Gly Val Thr Lys Val Gln Phe Ser Gln Tyr Asn Asp
               420   425   430

Arg Lys Asp Glu Val Arg Thr Gln Thr Tyr Asp Ser Lys Arg Asn Val
       435   440   445

Gly Gly Ile Val Phe Asp Ser Ile Asp Gln Leu Pro Pro Ile Thr Thr
       450   455   460

Asp Glu Ser Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Val Arg
465   470   475   480

Cys Phe Leu Leu Gln Gly Gly Arg Gly Ile Ile Pro Val Phe Thr Trp
               485   490   495

Thr His Lys Ser Val Asp Phe Tyr Asn Thr Leu Asp Ser Glu Lys Ile
               500   505   510

Thr Gln Ile Pro Phe Val Lys Ala Phe Ile Leu Val Asn Ser Thr Ser
               515   520   525

Val Val Ala Gly Pro Gly Phe Thr Gly Gly Asp Ile Ile Lys Cys Thr
       530   535   540

Asn Gly Ser Gly Leu Thr Leu Tyr Val Thr Pro Ala Pro Asp Leu Thr
545   550   555   560

Tyr Ser Lys Thr Tyr Lys Ile Arg Ile Arg Tyr Ala Ser Thr Ser Gln
               565   570   575

Val Arg Phe Gly Ile Asp Leu Gly Ser Tyr Thr His Ser Ile Ser Tyr
       580   585   590

Phe Asp Lys Thr Met Asp Lys Gly Asn Thr Leu Thr Tyr Asn Ser Phe

```
                595                        600                        605

      Asn Leu Ser Ser Val Ser Arg Pro Ile Glu Ile Ser Gly Gly Asn Lys
          610                 615                 620

      Ile Gly Val Ser Val Gly Gly Ile Gly Ser Gly Asp Glu Val Tyr Ile
      625                 630                 635                 640

      Asp Lys Ile Glu Phe Ile Pro Met Asp
                      645



      <210>  110
      <211>  652
      <212>  PRT
      <213>  Artificial sequence

      <220>
      <223>  Recombinant delta endotoxin

      <400>  110

      Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
      1               5                   10                  15

      Asn Ser Glu Leu Pro Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
                      20                  25                  30

      Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
                      35                  40                  45

      Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
          50                  55                  60

      Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
      65                  70                  75                  80

      Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                      85                  90                  95

      Asp Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
                      100                 105                 110

      Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
                      115                 120                 125

      Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
          130                 135                 140

      Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
      145                 150                 155                 160

      Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
                      165                 170                 175

      His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
                      180                 185                 190
```

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
        195   200   205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
        210   215   220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225   230   235   240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245   250   255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
        260   265   270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
        275   280   285

Val Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290   295   300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305   310   315   320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325   330   335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Ser
        340   345   350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
        355   360   365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370   375   380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385   390   395   400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
            405   410   415

Ile Tyr Phe Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
        420   425   430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
        435   440   445

His Val Gly Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
    450   455   460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465   470   475   480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
            485   490   495

```
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
        500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515         ·   520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
            565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Ile Val Ile
            580             585             590

Tyr Ile Asn Lys Thr Met Asn Ile Asp Asp Asp Leu Thr Tyr Gln Thr
        595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Thr
    610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
            645             650

<210>   111
<211>   652
<212>   PRT
<213>   Artificial sequence
<220>
<223>   Recombinant delta endotoxin

<400>   111

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1               5               10              15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20              25              30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
            35              40              45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
        50              55              60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65              70              75              80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
            85              90              95
```

```
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
            100             105             110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
            115             120             125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
    130             135             140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145             150             155                 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
            165             170             175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
            180             185             190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
            195             200             205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
    210             215             220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225             230             235                 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
            245             250             255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
            260             265             270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
            275             280             285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
    290             295             300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305             310             315             320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
            325             330             335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
            340             345             350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
            355             360             365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
    370             375             380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385             390             395             400
```

```
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
             405             410             415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
             420             425             430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
         435             440             445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
         450             455             460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465             470             475             480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
             485             490             495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
         500             505             510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
         515             520             525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
         530             535             540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545             550             555             560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
             565             570             575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
             580             585             590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
             595             600             605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
         610             615             620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625             630             635             640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
             645             650
```

```
<210>  112
<211>  659
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Recombinant delta endotoxin
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<400> 112

```
Met Ile Arg Met Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu
1               5               10              15

Tyr Asp Thr Ile Lys Val Thr Pro Asn Ser Glu Leu Pro Thr Asn His
            20              25              30

Asn Gln Tyr Pro Leu Ala Asp Asn Pro Asn Ser Thr Leu Glu Glu Leu
        35              40              45

Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Ser Thr Glu Val
    50              55              60

Leu Asp Ser Ser Thr Val Lys Asp Ala Val Gly Thr Gly Ile Ser Val
65              70              75              80

Val Gly Gln Ile Leu Gly Val Val Gly Val Pro Phe Ala Gly Ala Leu
            85              90              95

Thr Ser Phe Tyr Gln Ser Phe Leu Asn Ala Ile Trp Pro Ser Asp Ala
            100             105             110

Asp Pro Trp Lys Ala Phe Met Ala Gln Val Glu Val Leu Ile Asp Lys
        115             120             125

Lys Ile Glu Glu Tyr Ala Lys Ser Lys Ala Leu Ala Glu Leu Gln Gly
    130             135             140

Leu Gln Asn Asn Phe Glu Asp Tyr Val Asn Ala Leu Asp Ser Trp Lys
145             150             155             160

Lys Ala Pro Val Asn Leu Arg Ser Arg Arg Ser Gln Asp Arg Ile Arg
            165             170             175

Glu Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser
        180             185             190

Phe Ala Val Ser Lys Phe Glu Val Leu Phe Leu Pro Thr Tyr Ala Gln
        195             200             205

Ala Ala Asn Thr His Leu Leu Leu Leu Lys Asp Ala Gln Val Phe Gly
    210             215             220

Glu Glu Trp Gly Tyr Ser Ser Glu Asp Ile Ala Glu Phe Tyr Gln Arg
225             230             235             240

Gln Leu Lys Leu Thr Gln Gln Tyr Thr Asp His Cys Val Asn Trp Tyr
            245             250             255

Asn Val Gly Leu Asn Ser Leu Arg Gly Ser Thr Tyr Asp Ala Trp Val
        260             265             270

Lys Phe Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu
        275             280             285
```

```
Ile Val Leu Phe Pro Phe Tyr Asp Val Arg Leu Tyr Ser Lys Gly Val
    290                 295                 300

Lys Thr Glu Leu Thr Arg Asp Ile Phe Thr Asp Pro Ile Phe Thr Leu
305                 310                 315                 320

Asn Ala Leu Gln Glu Tyr Gly Pro Thr Phe Ser Ser Ile Glu Asn Ser
            325                 330                 335

Ile Arg Lys Pro His Leu Phe Asp Tyr Leu Arg Gly Ile Glu Phe His
            340                 345                 350

Thr Arg Leu Arg Pro Gly Tyr Ser Gly Lys Asp Ser Phe Asn Tyr Trp
            355                 360                 365

Ser Gly Asn Tyr Val Glu Thr Arg Pro Ser Ile Gly Ser Asn Asp Thr
    370                 375                 380

Ile Thr Ser Pro Phe Tyr Gly Asp Lys Ser Ile Glu Pro Ile Gln Lys
385                 390                 395                 400

Leu Ser Phe Asp Gly Gln Lys Val Tyr Arg Thr Ile Ala Asn Thr Asp
            405                 410                 415

Ile Ala Ala Phe Pro Asp Gly Lys Ile Tyr Phe Gly Val Thr Lys Val
            420                 425                 430

Asp Phe Ser Gln Tyr Asp Asp Gln Lys Asn Glu Thr Ser Thr Gln Thr
            435                 440                 445

Tyr Asp Ser Lys Arg Tyr Asn Gly Tyr Leu Gly Ala Gln Asp Ser Ile
    450                 455                 460

Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Ala Tyr
465                 470                 475                 480

Ser His Gln Leu Asn Tyr Ala Glu Cys Phe Leu Met Gln Asp Arg Arg
            485                 490                 495

Gly Thr Ile Pro Phe Phe Thr Trp Thr His Arg Ser Val Asp Phe Phe
            500                 505                 510

Asn Thr Ile Asp Ala Glu Lys Ile Thr Gln Leu Pro Val Val Lys Ala
            515                 520                 525

Tyr Ala Leu Ser Ser Gly Ala Ser Ile Ile Glu Gly Pro Gly Phe Thr
    530                 535                 540

Gly Gly Asn Leu Leu Phe Leu Lys Glu Ser Ser Asn Ser Ile Ala Lys
545                 550                 555                 560

Phe Lys Val Thr Leu Asn Ser Ala Ala Leu Leu Gln Arg Tyr Arg Val
            565                 570                 575

Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Arg Leu Phe Val Gln Asn
            580                 585                 590
```

```
Ser Asn Asn Asp Phe Leu Val Ile Tyr Ile Asn Lys Thr Met Asn Ile
        595             600             605

Asp Gly Asp Leu Thr Tyr Gln Thr Phe Asp Phe Ala Thr Ser Asn Ser
        610             615             620

Asn Met Gly Phe Ser Gly Asp Thr Asn Asp Phe Ile Ile Gly Ala Glu
625             630             635             640

Ser Phe Val Ser Asn Glu Lys Ile Tyr Ile Asp Lys Ile Glu Phe Ile
            645             650             655    .

Pro Val Gln


<210>  113
<211>  652
<212>  PRT
<213>  Artificial sequence
<220>
<223>  Recombinant delta endotoxin
<400>  113
Met Ile Arg Lys Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu
1                   5                   10                  15

His Asp Thr Ile Lys Thr Thr Glu Asn Asn Glu Val Pro Thr Asn His
            20              25              30

Val Gln Tyr Pro Leu Ala Glu Thr Pro Asn Pro Thr Leu Glu Asp Leu
        35              40              45

Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Asn Thr Glu Ala
    50              55              60

Leu Asp Ser Ser Thr Thr Lys Asp Val Ile Gln Lys Gly Ile Ser Val
65              70              75              80

Val Gly Asp Leu Leu Gly Val Val Gly Phe Pro Phe Gly Gly Ala Leu
            85              90              95

Val Ser Phe Tyr Thr Asn Phe Leu Asn Thr Ile Trp Pro Ser Glu Asp
            100             105             110

Pro Trp Lys Ala Phe Met Glu Gln Val Glu Ala Leu Met Asp Gln Lys
        115             120             125

Ile Ala Asp Tyr Ala Lys Asn Lys Ala Leu Ala Glu Leu Gln Gly Leu
    130             135             140

Gln Asn Asn Val Glu Asp Tyr Val Ser Ala Leu Ser Ser Trp Gln Lys
145             150             155             160

Asn Pro Val Ser Ser Arg Asn Pro His Ser Gln Gly Arg Ile Arg Glu
            165             170             175

Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser Phe
            180             185             190
```

```
Ala Ile Ser Gly Tyr Glu Val Leu Phe Leu Thr Thr Tyr Ala Gln Ala
        195             200             205

Ala Asn Thr His Leu Phe Leu Leu Lys Asp Ala Gln Ile Tyr Gly Glu
        210             215             220

Glu Trp Gly Tyr Glu Lys Glu Asp Ile Ala Glu Phe Tyr Lys Arg Gln
225             230             235             240

Leu Lys Leu Thr Gln Glu Tyr Thr Asp His Cys Val Lys Trp Tyr Asn
        245             250             255

Val Gly Leu Asp Lys Leu Arg Gly Ser Ser Tyr Glu Ser Trp Val Asn
        260             265             270

Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu Ile
        275             280             285

Ala Leu Phe Pro Leu Tyr Asp Val Arg Leu Tyr Pro Lys Glu Val Lys
        290             295             300

Thr Glu Leu Thr Arg Asp Val Leu Thr Asp Pro Ile Val Gly Val Asn
305             310             315             320

Asn Leu Arg Gly Tyr Gly Thr Thr Phe Ser Asn Ile Glu Asn Tyr Ile
        325             330             335

Arg Lys Pro His Leu Phe Asp Tyr Leu His Arg Ile Gln Phe His Thr
        340             345             350

Arg Phe Gln Pro Gly Tyr Tyr Gly Asn Asp Ser Phe Asn Tyr Trp Ser
        355             360             365

Gly Asn Tyr Val Ser Thr Arg Pro Ser Ile Gly Ser Asn Asp Ile Ile
        370             375             380

Thr Ser Pro Phe Tyr Gly Asn Lys Ser Ser Glu Pro Val Gln Asn Leu
385             390             395             400

Glu Phe Asn Gly Glu Lys Val Tyr Arg Ala Val Ala Asn Thr Asn Leu
            405             410             415

Ala Val Trp Pro Ser Ala Val Tyr Ser Gly Val Thr Lys Val Glu Phe
        420             425             430

Ser Gln Tyr Asn Asp Gln Thr Asp Glu Ala Ser Thr Gln Thr Tyr Asp
        435             440             445

Ser Lys Arg Asn Val Gly Ala Val Ser Trp Asp Ser Ile Asp Gln Leu
        450             455             460

Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Gly Tyr Ser His Gln
465             470             475             480

Leu Asn Tyr Val Met Cys Phe Leu Met Gln Gly Ser Arg Gly Thr Ile
            485             490             495
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Pro Val Leu Thr Trp Thr His Lys Ser Val Asp Phe Phe Asn Met Ile
            500   505   510

Asp Ser Lys Lys Ile Thr Gln Leu Pro Leu Val Lys Ala Tyr Lys Leu
            515   520   525

Gln Ser Gly Ala Ser Val Val Ala Gly Pro Arg Phe Thr Gly Gly Asp
        530   535   540

Ile Ile Gln Cys Thr Glu Asn Gly Ser Ala Ala Thr Ile Tyr Val Thr
545   550   555   560

Pro Asp Val Ser Tyr Ser Gln Lys Tyr Arg Ala Arg Ile His Tyr Ala
                565   570   575

Ser Thr Ser Gln Ile Thr Phe Thr Leu Ser Leu Asp Gly Ala Pro Phe
            580   585   590

Asn Gln Tyr Tyr Phe Asp Lys Thr Ile Asn Lys Gly Asp Thr Leu Thr
            595   600   605

Tyr Asn Ser Phe Asn Leu Ala Ser Phe Ser Thr Pro Phe Glu Leu Ser
            610   615   620

Gly Asn Asn Leu Gln Ile Gly Val Thr Gly Leu Ser Ala Gly Asp Lys
625   630   635   640

Val Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Asn
                645   650